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1A

The susceptibility of suckling rabbits to infection with coccidia. M. PAKANDL and L. HlÁSKOVÁ. Biology Centre, Academy of Science of Czech Republic, Institute of Parasitology, Branišovská 31, 37005 České Budějovice, Czech Republic.

Suckling rabbits from six litters were orally inoculated at various ages with oocysts of the precocious lines of *Eimeria flavescens* and *E. intestinalis* or with a mixture of these lines with wild strains of *E. media* and *E. magna*. The number of oocysts in the caeca served as the criterion of oocyst production. Rabbits younger than 23 days remained uninfected, whereas the number of oocysts in the caeca increased with the age of animals at inoculation. However, the oocyst output was markedly lower in all the animals before weaning compared with rabbits older than 6 weeks. The dependence of oocyst production on the age of inoculated rabbits was similar in all four Coccidian species.

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2A

Cysteine and aspartic peptidases from the gut of the tick *Ixodes ricinus*. D. SOJKA,[a] J. DVOŘÁK,[b] M. SAJID,[b] Z. FRANTA,[a] O. HAJDUŠEK,[a] C.R. CAFFREY[b] and P. KOPÁČEK[a]. [a]Biology Centre, Academy of Science of Czech Republic, Institute of Parasitology and Faculty of Biological Sciences, University of South Bohemia, České Budjovičě, [b]Sandler Center for Basic Research in Parasitic Diseases, University of California, San Francisco.

Despite its importance, our understanding of hemoglobin digestion in ticks is still very limited and lags far behind current knowledge of this process in other hematophagous parasites. Screening of gut-specific cDNA library from the hard tick *Ixodes ricinus* resulted in isolation of a gene coding for an asparaginyl endopeptidase (legumain) designated as IrAE which is to our knowledge the first member of cysteine peptidase family C13 of the CD clan described among arthropods. IrAE is an ortholog of asparaginyl endopeptidase from *Schistosoma mansoni*, which plays a pivotal role in the hemoglobin digestion by this parasite by trans-activation of other high-performance cysteine and aspartic peptidases (Caffrey et al., *Trends Parasitol.* 20: 241–8, 2004). In addition, using degenerated primers we have identified other orthologs of schistosomal proteases from a gut cDNA library of *I. ricinus*, cysteine endopeptidases cathepsin B, L, cysteine exopeptidase cathepsin C and aspartic peptidase cathepsin D. IrAE was expressed in *P. pastoris* and its enzymatic properties were performed with the use of aza-epoxide inhibitors, fluorescent substrates, and activity-based probes. IrAE seems to be the first peptidase reported to date to be secreted out of the tick digestive cells or is highly enriched on the surface of gut epithelium. Genes for other found peptidases are highly and specifically expressed in adult female guts after feeding on laboratory guinea-pigs. IrAE is potent to activate schistosomal cathepsin B1 in *trans* and to cleave hemoglobin at pH 4.0. These new findings show similarity in digestive proteolytic systems of blood flukes and ticks. Based on our data, we suggest cysteine and aspartic peptidases to be one of the key molecules of tick gut, having roles in blood digestion, production of eggs, pathogen–vector interactions, and production of antimicrobial peptides derived from host hemoglobin.

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3A

Phlebotomine sand flies in an endemic focus of cutaneous leishmaniasis in Turkey: identification of the vector. M. SVOBODOVÁ,[a] J. VOTÝPKA,[a] L. ZÍDKOVÁ,[a] J. HLAVAÈKOVÁ,[a] A. BELEN,[b] B. ALTEN[b] and P.VOLF[a]. [a]Department of Parasitology, Charles University, 128 44 Prague, Czech Republic, [b]Department of Biology, Hacettepe University, Ankara, Turkey.

Sand flies (Diptera: Psychodidae) were investigated as possible vectors of cutaneous leishmaniasis (CL) in a focus near Adana, South-East Anatolia, Turkey. CDC light traps were placed in houses and animal shelters in endemic villages; of 551 females dissected and identified 77% were *Phlebotomus tobbi*, and 15% were *P. papatasi*. Other species (*P. cf neglectus*, *P. sergenti*, *P. perfiliewi*) each represented less than 1% of sand fly fauna. In males the relative composition of species was similar. Two dissected females of *P. tobbi* (0.4%) harboured promastigotes in their gut. Typing (ITS1-PCR-RFLP using *Hae*III enzyme) revealed that both isolates are *Leishmania infantum*. Moreover, a strain isolated from a local patient with CL was identical with sand-fly isolates. *P.* (Larroussious) *tobbi* is thus considered as a vector of CL in this focus. To our knowledge, this is the first time that *L. infantum* was isolated in a CL focus from both, *P. tobbi* and human patient.

4A

A parsimonious hypothesis for the origin of the eukaryotic nucleus. M. VESTEG, J. KRAJČOVIČ and L. EBRINGER. Institute of Cell Biology, Faculty of Natural Sciences, Comenius University, 842 15 Bratislava, Slovakia.

The most common hypothesis for the origin of eukaryotic cell suggests a symbiosis of an α-proteobacterium in an archaeal cell. Another favorite hypothesis proposes endosymbiotic origin of the nucleus from an archaeal symbiont in a bacterium. Other hypotheses suppose a phagothrophic origin of eukaryotes. The major problems of such hypotheses are e.g. the substitution of an archaeal membrane by a bacterial one, multiply symbiogenesis, and origin of eukaryote-specific phagotrophy before the origin of eukaryotes. Our new hypothesis focusing on the origin of the nucleus resolves all these problems and tries to minimize the number of hardly explainable steps leading to the first eukaryote. In our view the host entity involved in eukaryote-creating symbiogenesis was neither an archaeal cell nor a bacterium but rather a different (pre-karyotic) lineage. The pre-karyote possessed an outer and inner membrane of bacterial type (like G^--bacteria), while it possessed archaeal-like informational apparatus. An α-proteobacterial-like symbiont invaded the periplasmic space between the two membranes. The host-symbiont coevolution resulted later in irreversible enclosure of the symbiont in the host periplasm and the transformation of the host periplasm to eukaryotic cytoplasm. Under this hypothesis the pre-karyote inner membrane was the ancestor of eukaryotic nuclear membrane, endoplasmic reticulum, and Golgi apparatus. These suggestions seem to be compatible with the theory of membrane heredity. The origin of the pre-karyote could be easily explained by Woese's arguments about the communal nature of the universal ancestor. In addition, *B. dellovibrio* represents an example of an extant periplamic parasite.